

SEQUENCE LISTING

<110> Dale L. Ludwig

<120> Fully Human Antibodies Directed Against the Human Insulin-Like Growth Factor-1 Receptor

<130> 11245/53202

<140> To Be Assigned

<141> Herewith...2005-11-01

<150> PCT/US2004/013852

<151> 2004-05-03

<150> US 60/467,177

<151> 2003-05-01

<160> 33

<170> PatentIn version 3.3

<210> 1

<211> 390

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(390)

<400> 1

gag gtc	cag ctg	gtg cag	tct ggg	gct gag	gtg aag	aag cct	ggg tcc	48
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1		5		10		15		

tcg gtg	aag gtc	tcc tgc	aag gct	tct gga	ggc acc	ttc agc	agc agc	tat	96
Ser Val	Lys Val	Ser Cys	Lys Ala	Ser Gly	Gly Thr	Phe Ser	Ser Ser	Tyr	
	20		25			30			

gct atc	agc tgg	gtg cga	cag gcc	cct gga	caa ggg	ctt gag	tgg atg	144
Ala Ile	Ser Trp	Val Arg	Gln Ala	Pro Gly	Gln Gly	Leu Glu	Trp Met	
	35		40		45			

gga ggg	atc atc	cct atc	ttt ggt	aca gca	aac tac	gca cag	aag ttc	192
Gly Gly	Ile Ile	Pro Ile	Phe Gly	Thr Ala	Asn Tyr	Ala Gln	Lys Phe	
50			55		60			

dag ggc	aga gtc	acg att	acc gcg	gac aaa	tcc acg	agc aca	gcc tac	240
Gln Gly	Arg Val	Thr Ile	Thr Ala	Asp Lys	Ser Thr	Ser Thr	Ala Tyr	
65		70		75		80		

atg gag	ctg agc	agc ctg	aga tct	gag gac	acg gcc	gtg tat	tac tgt	288
Met Glu	Leu Ser	Ser Leu	Arg Ser	Glu Asp	Thr Ala	Val Tyr	Tyr Cys	
	85		90		95			

gcg aga	gcg cca	tta cga	ttt ttg	gag tgg	tcc acc	caa gac	cac tac	336
Ala Arg	Ala Pro	Leu Arg	Phe Leu	Glu Trp	Ser Thr	Gln Asp	His Tyr	
	100		105		110			

tac	tac	tac	tac	atg	gac	gtc	tgg	ggc	aaa	ggg	acc	acg	gtc	acc	gtc	384
Tyr	Tyr	Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	
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tca	agc	390
Ser	Ser	
	130	

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<400> 2

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Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
			20					25					30		

Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			

Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55					60				

Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Ala	Arg	Ala	Pro	Leu	Arg	Phe	Leu	Glu	Trp	Ser	Thr	Gln	Asp	His	Tyr
			100					105					110		

Tyr	Tyr	Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val
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Ser	Ser
	130

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<220>
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gta cat tca gag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag	96
Val His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc	144
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe	
35 40 45	
agc agc tat gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt	192
Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
50 55 60	
gag tgg atg gga ggg atc atc cct atc ttt ggt aca gca aac tac gca	240
Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala	
65 70 75 80	
cag aag ttc cag ggc aga gtc acg att acc gcg gac aaa tcc acg agc	288
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser	
85 90 95	
aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gcg aga gcg cca tta cga ttt ttg gag tgg tcc acc caa	384
Tyr Tyr Cys Ala Arg Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln	
115 120 125	
gac cac tac tac tac tac tac atg gac gtc tgg ggc aaa ggg acc acg	432
Asp His Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr	
130 135 140	
gtc acc gtc tca agc gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg	480
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu	
145 150 155 160	
gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc	528
Ala Pro Ser Ser Lys Ser Thr Ser Gly Thr Ala Ala Leu Gly Cys	
165 170 175	
ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca	576
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser	
180 185 190	
ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc	624
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser	
195 200 205	
tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	672
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser	
210 215 220	
ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	720
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn	
225 230 235 240	

acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt gac aaa act cac	768
Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His	
245 250 255	
aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc	816
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val	
260 265 270	
ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc	864
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr	
275 280 285	
cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag	912
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu	
290 295 300	
gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag	960
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys	
305 310 315 320	
aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc	1008
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser	
325 330 335	
gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag	1056
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys	
340 345 350	
tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc	1104
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile	
355 360 365	
tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc	1152
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro	
370 375 380	
cca tcc ccg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg	1200
Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu	
385 390 395 400	
gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat	1248
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn	
405 410 415	
ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc	1296
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser	
420 425 430	
gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg	1344
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg	
435 440 445	
tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg	1392
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu	
450 455 460	
cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga	1440
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
465 470 475	

<210> 4
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<212> PRT
<213> Homo sapiens

<400> 4

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
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20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
35 40 45

Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala
65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln
115 120 125

Asp His Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr
130 135 140

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
145 150 155 160

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
165 170 175

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
180 185 190

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
195 200 205

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser

210		215		220
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn				
225		230		235 240
Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His				
	245		250	255
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val				
	260		265	270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr				
	275		280	285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu				
	290		295	300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys				
305		310		315 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser				
	325		330	335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys				
	340		345	350
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile				
	355		360	365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro				
	370		375	380
Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu				
385		390		395 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn				
	405		410	415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser				
	420		425	430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg				
	435		440	445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu				
	450		455	460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 465 470 475

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<220>
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 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
 20 25 30
 agc tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat 144
 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 ggt aaa aac aac cgg ccc tca ggg atc cca gac cga ttc tct ggc tcc 192
 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
 50 55 60
 agc tca gga aac aca gct tcc ttg acc atc act ggg gct cag gcg gaa 240
 Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65 70 75 80
 gat gag gct gac tat tac tgt aac tcc cgg gac aac agt gat aac cgt 288
 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Asn Ser Asp Asn Arg
 85 90 95
 ctg ata ttt ggc ggc ggg acc aag ctg acc gtc ctc agt 327
 Leu Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser
 100 105

<210> 6
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 6
 Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
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 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
 20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
 50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Asn Ser Asp Asn Arg
 85 90 95

Leu Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser
 100 105

<210> 7
 <211> 702
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(702)

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 gta cat tca tct tct gag ctg act cag gac cct gct gtg tct gtg gcc 96
 Val His Ser Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala
 20 25 30
 ttg gga cag aca gtc agg atc aca tgc caa gga gac agc ctc aga agc 144
 Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser
 35 40 45
 tat tat gca agc tgg tac cag cag aag cca gga cag gcc cct gta ctt 192
 Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu
 50 55 60
 gtc atc tat ggt aaa aac aac cgg ccc tca ggg atc cca gac cga ttc 240
 Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe
 65 70 75 80
 tct ggc tcc agc tca gga aac aca gct tcc ttg acc atc act ggg gct 288
 Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala
 85 90 95
 cag gcg gaa gat gag gct gac tat tac tgt aac tcc cgg gac aac agt 336
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Asn Ser
 100 105 110
 gat aac cgt ctg ata ttt ggc ggc ggg acc aag ctg acc gtc ctc agt 384
 Asp Asn Arg Leu Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser

115	120	125	
cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag			432
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu			
130	135	140	
gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc			480
Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe			
145	150	155	160
tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc gtc			528
Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val			
	165	170	175
aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag			576
Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys			
	180	185	190
tac gcg gcc agc agc tat ctg agc ctg acg cct gag cag tgg aag tcc			624
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser			
	195	200	205
cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag			672
His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu			
	210	215	220
aag aca gtg gcc cct gca gaa tgc tct tga			702
Lys Thr Val Ala Pro Ala Glu Cys Ser			
225	230		

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<400> 8

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Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser		
	35	45
Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu		
	50	60
Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe		
65	70	80
Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala		
	85	95

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Asn Ser
 100 105 110

Asp Asn Arg Leu Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser
 115 120 125

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
 130 135 140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 145 150 155 160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
 165 170 175

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
 180 185 190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
 195 200 205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
 210 215 220

Lys Thr Val Ala Pro Ala Glu Cys Ser
 225 230

<210> 9
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<220>
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<400> 9
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 aca gtc agg atc aca tgc caa gga gac agc ctc aga agc tat tat gca 96
 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
 20 25 30
 acc tgg tac cag cag aag cca gga cag gcc cct att ctt gtc atc tat 144
 Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu Val Ile Tyr
 35 40 45
 ggt gaa aat aag cgg ccc tca ggg atc cca gac cga ttc tct ggc tcc 192

Gly	Glu	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser		
50						55					60						
agc	tca	gga	aac	aca	gct	tcc	ttg	acc	atc	act	ggg	gct	cag	gca	gaa		240
Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu		
65					70					75					80		
gat	gag	gct	gac	tac	tat	tgt	aaa	tct	cgg	gat	ggc	agt	ggg	caa	cat		288
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Lys	Ser	Arg	Asp	Gly	Ser	Gly	Gln	His		
				85					90					95			
ctg	gtg	ttc	ggc	gga	ggg	acc	aag	ctg	acc	gtc	cta	ggg					327
Leu	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly					
			100					105									

<210> 10
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 <212> PRT
 <213> Homo sapiens

<400> 10

Ser	Ser	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln		
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Thr	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala		
			20					25					30				

Thr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Ile	Leu	Val	Ile	Tyr		
		35					40					45					

Gly	Glu	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser		
50						55					60						

Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu		
65					70					75					80		

Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Lys	Ser	Arg	Asp	Gly	Ser	Gly	Gln	His		
				85					90					95			

Leu	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly					
			100					105									

<210> 11
 <211> 702
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(702)

<400> 11

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gta cat tca tct tct gag ctg act cag gac cct gct gtg tct gtg gcc	96
Val His Ser Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala	
20 25 30	
ttg gga cag aca gtc agg atc aca tgc caa gga gac agc ctc aga agc	144
Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser	
35 40 45	
tat tat gca acc tgg tac cag cag aag cca gga cag gcc cct att ctt	192
Tyr Tyr Ala Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu	
50 55 60	
gtc atc tat ggt gaa aat aag cgg ccc tca ggg atc cca gac cga ttc	240
Val Ile Tyr Gly Glu Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe	
65 70 75 80	
tct ggc tcc agc tca gga aac aca gct tcc ttg acc atc act ggg gct	288
Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala	
85 90 95	
cag gca gaa gat gag gct gac tac tat tgt aaa tct cgg gat ggc agt	336
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Lys Ser Arg Asp Gly Ser	
100 105 110	
ggt caa cat ctg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt	384
Gly Gln His Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly	
115 120 125	
cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag	432
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu	
130 135 140	
gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc	480
Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe	
145 150 155 160	
tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc gtc	528
Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val	
165 170 175	
aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag	576
Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys	
180 185 190	
tac gcg gcc agc agc tat ctg agc ctg acg cct gag cag tgg aag tcc	624
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser	
195 200 205	
cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag	672
His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu	
210 215 220	
aag aca gtg gcc cct gca gaa tgc tct tga	702
Lys Thr Val Ala Pro Ala Glu Cys Ser	
225 230	

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<400> 12

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
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Val His Ser Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala
20 25 30

Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser
35 40 45

Tyr Tyr Ala Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu
50 55 60

Val Ile Tyr Gly Glu Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe
65 70 75 80

Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala
85 90 95

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Lys Ser Arg Asp Gly Ser
100 105 110

Gly Gln His Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
115 120 125

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
130 135 140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
145 150 155 160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
165 170 175

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
180 185 190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
195 200 205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu

210

215

220

Lys Thr Val Ala Pro Ala Glu Cys Ser
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 Ser Tyr Ala Ile Ser
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15

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48

ggc
 Gly

51

<210> 16
 <211> 17
 <212> PRT
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<400> 16

Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

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 <211> 63
 <212> DNA
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<220>
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 Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln Asp His Tyr Tyr Tyr
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tac tac atg gac gtc 63
 Tyr Tyr Met Asp Val
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Tyr Tyr Met Asp Val
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21

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Gly Lys Asn Asn Arg Pro Ser
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<210> 23
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33

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<212> PRT
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<400> 24

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1 5 10

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Gly Glu Asn Lys Arg Pro Ser
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21

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Gly Glu Asn Lys Arg Pro Ser
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 Lys Ser Arg Asp Gly Ser Gly Gln His Leu Val
 1 5 10

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<400> 31
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<400> 32
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